



SEQUENCE LISTING

<110> Yanofsky, Martin F.
Liljegren, Sarah
The Regents of the University of California

<120> Selective Control of Lignin Biosynthesis in Transgenic Plants

<130> 19452A-000930US

<140> US 09/978,382
<141> 2001-10-15

<150> US 60/090,649
<151> 1998-06-25

<150> US 09/339,998
<151> 1999-06-25

<160> 25

<170> PatentIn Ver. 2.1

<210> 1
<211> 1062
<212> DNA
<213> Arabidopsis sp.

<220>
<221> CDS
<222> (101)..(829)
<223> AGAMOUS-LIKE 8 (AGL8)

<400> 1
cccagagaga cataagaaag aaagagagag agagatactt tggtcatttc agggttgtcg 60
tttctctctc ttgttcttga gattttgaag agagagagat atg gga aga ggt agg 115
Met Gly Arg Gly Arg
1 5
ggt cag ctg aag agg ata gag aac aag atc aat agg caa gtt act ttc 163
Val Gln Leu Lys Arg Ile Glu Asn Lys Ile Asn Arg Gln Val Thr Phe
10 15 20
tca aag aga agg tct ggt ttg ctc aag aaa gct cat gag atc tct gtt 211
Ser Lys Arg Arg Ser Gly Leu Leu Lys Lys Ala His Glu Ile Ser Val
25 30 35
ctc tgc gat gct gag gtt gct ctc atc gtc ttc tct tcc aaa ggc aaa 259
Leu Cys Asp Ala Glu Val Ala Leu Ile Val Phe Ser Ser Lys Gly Lys
40 45 50
ctc ttc gaa tat tcc acc gac tct tgc atg gag agg ata ctt gaa cgc 307
Leu Phe Glu Tyr Ser Thr Asp Ser Cys Met Glu Arg Ile Leu Glu Arg
55 60 65
tat gat cgc tat tta tat tca gac aaa caa ctt gtt ggc cga gac gtt 355
Tyr Asp Arg Tyr Leu Tyr Ser Asp Lys Gln Leu Val Gly Arg Asp Val
70 75 80 85

tca caa agt gaa aat tgg gtt cta gaa cat gct aag ctc aag gca aga 403
 Ser Gln Ser Glu Asn Trp Val Leu Glu His Ala Lys Leu Lys Ala Arg
 90 95 100
 gtt gag gta ctt gag aag aac aaa agg aat ttt atg ggg gaa gat ctt 451
 Val Glu Val Leu Glu Lys Asn Lys Arg Asn Phe Met Gly Glu Asp Leu
 105 110 115
 gat tcg ttg agc ttg aag gag ctc caa agc ttg gag cat cag ctc gat 499
 Asp Ser Leu Ser Leu Lys Glu Leu Gln Ser Leu Glu His Gln Leu Asp
 120 125 130
 gca gct atc aag agc att agg tca aga aag aac caa gct atg ttc gaa 547
 Ala Ala Ile Lys Ser Ile Arg Ser Arg Lys Asn Gln Ala Met Phe Glu
 135 140 145
 tcc ata tct gcg ctc cag aag aag gat aaa gcc ttg caa gat cac aac 595
 Ser Ile Ser Ala Leu Gln Lys Lys Asp Lys Ala Leu Gln Asp His Asn
 150 155 160 165
 aat tcg ctt ctc aaa aag att aag gag agg gag aag aaa acg ggt cag 643
 Asn Ser Leu Leu Lys Lys Ile Lys Glu Arg Glu Lys Lys Thr Gly Gln
 170 175 180
 caa gaa gga caa tta gtc caa tgc tcc aac tct tct tca gtt ctt ctg 691
 Gln Glu Gly Gln Leu Val Gln Cys Ser Asn Ser Ser Ser Val Leu Leu
 185 190 195
 cct caa tac tgc gta acc tcc tcc aga gat ggc ttt gtg gag aga gtt 739
 Pro Gln Tyr Cys Val Thr Ser Ser Arg Asp Gly Phe Val Glu Arg Val
 200 205 210
 ggg gga gag aac ggt ggt gca tcg tcg ttg acg gaa cca aac tct ctg 787
 Gly Gly Glu Asn Gly Gly Ala Ser Ser Leu Thr Glu Pro Asn Ser Leu
 215 220 225
 ctt ccg gct tgg atg tta cgt cct acc act acg aac gag tag 829
 Leu Pro Ala Trp Met Leu Arg Pro Thr Thr Thr Asn Glu
 230 235 240
 aactatctca ctctttataa tataatgata atataattaa tgtttaatat tttcataaca 889
 ttcagcattt ttttggtgac ttatactcat tattaataacc gatatgtttt agctagtcat 949
 attatatgta tgatggaact ccgttgctga gacgtatgta cgtaagctat cattagattc 1009
 actgcgtctt aagaacaaag attcatatct tggtaatgat ttctcatgaa ata 1062

<210> 2

<211> 242

<212> PRT

<213> Arabidopsis sp.

<400> 2

Met Gly Arg Gly Arg Val Gln Leu Lys Arg Ile Glu Asn Lys Ile Asn
 1 5 10 15
 Arg Gln Val Thr Phe Ser Lys Arg Arg Ser Gly Leu Leu Lys Lys Ala
 20 25 30
 His Glu Ile Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Val Phe
 35 40 45

Ser Ser Lys Gly Lys Leu Phe Glu Tyr Ser Thr Asp Ser Cys Met Glu
50 55 60
Arg Ile Leu Glu Arg Tyr Asp Arg Tyr Leu Tyr Ser Asp Lys Gln Leu
65 70 75 80
Val Gly Arg Asp Val Ser Gln Ser Glu Asn Trp Val Leu Glu His Ala
85 90 95
Lys Leu Lys Ala Arg Val Glu Val Leu Glu Lys Asn Lys Arg Asn Phe
100 105 110
Met Gly Glu Asp Leu Asp Ser Leu Ser Leu Lys Glu Leu Gln Ser Leu
115 120 125
Glu His Gln Leu Asp Ala Ala Ile Lys Ser Ile Arg Ser Arg Lys Asn
130 135 140
Gln Ala Met Phe Glu Ser Ile Ser Ala Leu Gln Lys Lys Asp Lys Ala
145 150 155 160
Leu Gln Asp His Asn Asn Ser Leu Leu Lys Lys Ile Lys Glu Arg Glu
165 170 175
Lys Lys Thr Gly Gln Gln Glu Gly Gln Leu Val Gln Cys Ser Asn Ser
180 185 190
Ser Ser Val Leu Leu Pro Gln Tyr Cys Val Thr Ser Ser Arg Asp Gly
195 200 205
Phe Val Glu Arg Val Gly Gly Glu Asn Gly Gly Ala Ser Ser Leu Thr
210 215 220
Glu Pro Asn Ser Leu Leu Pro Ala Trp Met Leu Arg Pro Thr Thr Thr
225 230 235 240
Asn Glu

<210> 3
<211> 896
<212> DNA
<213> Arabidopsis sp.

<220>
<221> CDS
<222> (7)..(753)
<223> AGAMOUS-LIKE 1 (AGL1)

<400> 3
ggatca atg gag gaa ggt ggg agt agt cac gac gca gag agt agc aag 48
Met Glu Glu Gly Gly Ser Ser His Asp Ala Glu Ser Ser Lys
1 5 10
aaa cta ggg aga ggg aaa ata gag ata aag agg ata gag aac aca aca 96
Lys Leu Gly Arg Gly Lys Ile Glu Ile Lys Arg Ile Glu Asn Thr Thr
15 20 25 30
aat cgt caa gtt act ttc tgc aaa cga cgc aat ggt ctt ctc aag aaa 144
Asn Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Leu Lys Lys
35 40 45
gct tat gaa ctc tct gtc ttg tgt gat gcc gaa gtt gcc ctc gtc atc 192
Ala Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Val Ile
50 55 60
ttc tcc act cgt ggc cgt ctc tat gag tac gcc aac aac agt gtg agg 240
Phe Ser Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn Ser Val Arg
65 70 75
ggc aca att gaa agg tac aag aaa gct tgt tcc gat gcc gtc aac cct 288
Gly Thr Ile Glu Arg Tyr Lys Lys Ala Cys Ser Asp Ala Val Asn Pro
80 85 90

cct tcc gtc acc gaa gct aat act cag tac tat cag caa gaa gcc tct 336
 Pro Ser Val Thr Glu Ala Asn Thr Gln Tyr Tyr Gln Gln Glu Ala Ser
 95 100 105 110

 aag ctt cgg agg cag att cga gat att cag aat tca aat agg cat att 384
 Lys Leu Arg Arg Gln Ile Arg Asp Ile Gln Asn Ser Asn Arg His Ile
 115 120 125

 gtt ggg gaa tca ctt ggt tcc ttg aac ttc aag gaa ctc aaa aac cta 432
 Val Gly Glu Ser Leu Gly Ser Leu Asn Phe Lys Glu Leu Lys Asn Leu
 130 135 140

 gaa gga cgt ctt gaa aaa gga atc agc cgt gtc cgc tcc aaa aag aat 480
 Glu Gly Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser Lys Lys Asn
 145 150 155

 gag ctg tta gtg gca gag ata gag tat atg cag aag agg gaa atg gag 528
 Glu Leu Leu Val Ala Glu Ile Glu Tyr Met Gln Lys Arg Glu Met Glu
 160 165 170

 ttg caa cac aat aac atg tac ctg cga gca aag ata gcc gaa ggc gcc 576
 Leu Gln His Asn Asn Met Tyr Leu Arg Ala Lys Ile Ala Glu Gly Ala
 175 180 185 190

 aga ttg aat ccg gac cag cag gaa tcg agt gtg ata caa ggg acg aca 624
 Arg Leu Asn Pro Asp Gln Gln Glu Ser Ser Val Ile Gln Gly Thr Thr
 195 200 205

 gtt tac gaa tcc ggt gta tct tct cat gac cag tcg cag cat tat aat 672
 Val Tyr Glu Ser Gly Val Ser Ser His Asp Gln Ser Gln His Tyr Asn
 210 215 220

 cgg aac tat att ccg gtg aac ctt ctt gaa ccg aat cag caa ttc tcc 720
 Arg Asn Tyr Ile Pro Val Asn Leu Leu Glu Pro Asn Gln Gln Phe Ser
 225 230 235

 ggc caa gac caa cct cct ctt caa ctt gtg taa ctcaaaacat gataacttgt 773
 Gly Gln Asp Gln Pro Pro Leu Gln Leu Val
 240 245

 ttcttccccct cataacgatt aagagagaga cgagagaggtt catttttatat ttataacgcg 833
 actgtgtatt catagttag gttctaataa tgataataac aaaactgttg tttctttgct 893
 tca 896

<210> 4

<211> 248

<212> PRT

<213> Arabidopsis sp.

<400> 4

Met Glu Glu Gly Gly Ser Ser His Asp Ala Glu Ser Ser Lys Lys Leu
 1 5 10 15
 Gly Arg Gly Lys Ile Glu Ile Lys Arg Ile Glu Asn Thr Thr Asn Arg
 20 25 30
 Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala Tyr
 35 40 45
 Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Val Ile Phe Ser
 50 55 60

```

Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn Ser Val Arg Gly Thr
65      70      75      80
Ile Glu Arg Tyr Lys Lys Ala Cys Ser Asp Ala Val Asn Pro Pro Ser
      85      90      95
Val Thr Glu Ala Asn Thr Gln Tyr Tyr Gln Gln Glu Ala Ser Lys Leu
      100      105      110
Arg Arg Gln Ile Arg Asp Ile Gln Asn Ser Asn Arg His Ile Val Gly
      115      120      125
Glu Ser Leu Gly Ser Leu Asn Phe Lys Glu Leu Lys Asn Leu Glu Gly
      130      135      140
Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser Lys Lys Asn Glu Leu
145      150      155      160
Leu Val Ala Glu Ile Glu Tyr Met Gln Lys Arg Glu Met Glu Leu Gln
      165      170      175
His Asn Asn Met Tyr Leu Arg Ala Lys Ile Ala Glu Gly Ala Arg Leu
      180      185      190
Asn Pro Asp Gln Gln Glu Ser Ser Val Ile Gln Gly Thr Thr Val Tyr
      195      200      205
Glu Ser Gly Val Ser Ser His Asp Gln Ser Gln His Tyr Asn Arg Asn
      210      215      220
Tyr Ile Pro Val Asn Leu Leu Glu Pro Asn Gln Gln Phe Ser Gly Gln
225      230      235      240
Asp Gln Pro Pro Leu Gln Leu Val
      245

```

<210> 5
 <211> 959
 <212> DNA
 <213> Arabidopsis sp.

<220>
 <221> CDS
 <222> (78)..(818)
 <223> AGAMOUS-LIKE 5 (AGL5)

```

<400> 5
gaattcatct tcccatcctc acttctcttt ctttctgatc ataattaatc ttgctaagcc 60

agctagggct tatagaa atg gag ggt ggt gcg agt aat gaa gta gca gag      110
          Met Glu Gly Gly Ala Ser Asn Glu Val Ala Glu
              1              5              10

agc agc aag aag ata ggg aga ggg aag ata gag ata aag agg ata gag      158
Ser Ser Lys Lys Ile Gly Arg Gly Lys Ile Glu Ile Lys Arg Ile Glu
          15              20              25

aac act acg aat cgt caa gtc act ttc tgc aaa cga cgc aat ggt tta      206
Asn Thr Thr Asn Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu
          30              35              40

ctc aag aaa gct tat gag ctc tct gtc ttg tgt gac gct gag gtt gct      254
Leu Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala
          45              50              55

ctt gtc atc ttc tcc act cga ggc cgt ctc tac gag tac gcc aac aac      302
Leu Val Ile Phe Ser Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn
          60              65              70              75

```

```

agt gtg aga gga aca ata gaa agg tac aag aaa gct tgc tcc gac gcc 350
Ser Val Arg Gly Thr Ile Glu Arg Tyr Lys Lys Ala Cys Ser Asp Ala
      80                      85                      90

ggt aac cct ccg acc atc acc gaa gct aat act cag tac tat cag caa 398
Val Asn Pro Pro Thr Ile Thr Glu Ala Asn Thr Gln Tyr Tyr Gln Gln
      95                      100                      105

gag gcg tct aaa ctc cgg aga cag att cgg gac att cag aat ttg aac 446
Glu Ala Ser Lys Leu Arg Arg Gln Ile Arg Asp Ile Gln Asn Leu Asn
      110                      115                      120

aga cac att ctt ggt gaa tct ctt ggt tcc ttg aac ttt aag gaa ctc 494
Arg His Ile Leu Gly Glu Ser Leu Gly Ser Leu Asn Phe Lys Glu Leu
      125                      130                      135

aag aac ctt gaa agt agg ctt gag aaa gga atc agt cgt gtc cga tcc 542
Lys Asn Leu Glu Ser Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser
      140                      145                      150                      155

aag aag cac gag atg tta gtt gca gag att gaa tac atg caa aaa agg 590
Lys Lys His Glu Met Leu Val Ala Glu Ile Glu Tyr Met Gln Lys Arg
      160                      165                      170

gaa atc gag ctg caa aac gat aac atg tat ctc cgc tcc aag att act 638
Glu Ile Glu Leu Gln Asn Asp Asn Met Tyr Leu Arg Ser Lys Ile Thr
      175                      180                      185

gaa aga aca ggt cta cag caa caa gaa tcg agt gtg ata cat caa ggg 686
Glu Arg Thr Gly Leu Gln Gln Glu Ser Ser Val Ile His Gln Gly
      190                      195                      200

aca gtt tac gag tcg ggt gtt act tct tct cac cag tcg ggg cag tat 734
Thr Val Tyr Glu Ser Gly Val Thr Ser Ser His Gln Ser Gly Gln Tyr
      205                      210                      215

aac cgg aat tat att gcg gtt aac ctt ctt gaa ccg aat cag aat tcc 782
Asn Arg Asn Tyr Ile Ala Val Asn Leu Leu Glu Pro Asn Gln Asn Ser
      220                      225                      230                      235

tcc aac caa gac caa cca cct ctg caa ctt gtt tga ttcagtctaa 828
Ser Asn Gln Asp Gln Pro Pro Leu Gln Leu Val
      240                      245

cataagcttc tttcctcagc ctgagatcga tctatagtgt cacctaaatg cggccgcgtc 888

cctcaacatc tagtcgcaag ctgaggggaa ccactagtgt catacgaacc tccaagagac 948

ggttacacaa a 959

```

<210> 6

<211> 246

<212> PRT

<213> Arabidopsis sp.

<400> 6

```

Met Glu Gly Gly Ala Ser Asn Glu Val Ala Glu Ser Ser Lys Lys Ile
  1                      5                      10                      15
Gly Arg Gly Lys Ile Glu Ile Lys Arg Ile Glu Asn Thr Thr Asn Arg
      20                      25                      30

```

Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala Tyr
 35 40 45
 Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Val Ile Phe Ser
 50 55 60
 Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn Ser Val Arg Gly Thr
 65 70 75 80
 Ile Glu Arg Tyr Lys Lys Ala Cys Ser Asp Ala Val Asn Pro Pro Thr
 85 90 95
 Ile Thr Glu Ala Asn Thr Gln Tyr Tyr Gln Gln Glu Ala Ser Lys Leu
 100 105 110
 Arg Arg Gln Ile Arg Asp Ile Gln Asn Leu Asn Arg His Ile Leu Gly
 115 120 125
 Glu Ser Leu Gly Ser Leu Asn Phe Lys Glu Leu Lys Asn Leu Glu Ser
 130 135 140
 Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser Lys Lys His Glu Met
 145 150 155 160
 Leu Val Ala Glu Ile Glu Tyr Met Gln Lys Arg Glu Ile Glu Leu Gln
 165 170 175
 Asn Asp Asn Met Tyr Leu Arg Ser Lys Ile Thr Glu Arg Thr Gly Leu
 180 185 190
 Gln Gln Gln Glu Ser Ser Val Ile His Gln Gly Thr Val Tyr Glu Ser
 195 200 205
 Gly Val Thr Ser Ser His Gln Ser Gly Gln Tyr Asn Arg Asn Tyr Ile
 210 215 220
 Ala Val Asn Leu Leu Glu Pro Asn Gln Asn Ser Ser Asn Gln Asp Gln
 225 230 235 240
 Pro Pro Leu Gln Leu Val
 245

<210> 7
 <400> 7
 000

<210> 8
 <400> 8
 000

<210> 9
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification primer AGL8 5-gamma

<400> 9
 ccgtcgacga tgggaagagg taggggt

27

<210> 10
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification primer OAM14

<400> 10
aatcattacc aagatatgaa 20

<210> 11
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer

<400> 11
cggatagctc gaatatcg 18

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer

<400> 12
aaccattgcg tcgtttgc 18

<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer

<400> 13
gtaattacca ggcaaggact ctcc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer

<400> 14
gtcatcggcg ggggtcataa cgtg 24

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification primer

<400> 15
 gaggatagag aacactacga atcg 24

<210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification primer

<400> 16
 cagggtcaagt caatagattc 20

<210> 17
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification primer

<400> 17
 cagaatttag tgaataatat tg 22

<210> 18
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification oligonucleotide primer

<400> 18
 ggagatctga attcatcttc ccatcc 26

<210> 19
 <211> 65
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification oligonucleotide primer

<400> 19
 ccggtacctc aaacaagttg cagaggtggt tgggtcttgggt tggaggaatt ctgattcggt 60
 tcaag 65

<210> 20
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR genotyping
 AGL1 transgene-specific oligonucleotide

<400> 20
 gaaggtggga gtagtcacga c 21

<210> 21
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR genotyping
 AGL1 transgene-specific oligonucleotide

<400> 21
 cggaaggagg gttgacggca 20

<210> 22
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR genotyping
 AGL5 transgene-specific oligonucleotide

<400> 22
 ggtggtgcga gtaatgaagt a 21

<210> 23
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR genotyping
 AGL5 transgene-specific oligonucleotide

<400> 23
 tggtcggagg gttaacggcg 20

<210> 24
 <211> 3842
 <212> DNA
 <213> Arabidopsis sp.

<220>

<221> CDS

<222> (2758)..(3354)

<223> R-like basic heix-loop-helix transcription factor
(R-like bHLH)

<400> 24

```

ccatctacta tccggttggt gacccttaaa gcttttgaag actactagaa taatgcaa 60
accatattgtc catatccatc cttttctttt gtttgaactg aacattctaa ttttgtaaaa 120
gaaaaaacct tatgttaata tcaccgtagg caaaaaaaat atctcatcat attaaatttt 180
tattataaga ttatacattc tctcgttgta agagttactc caattgcaag tgttgtatta 240
actaataaaa aggacgaaag taggaagctt ataattaatt gatgttgcat agtactggta 300
tattgttgat gaatataaca agtatgaaca ttaatgcatg aaacggggta ttttgtcttg 360
aactcattaa aggcaatgtg aaaagaagat gtgagggtctc attttgaaaa tttatcttct 420
agctttgtcg attttaaatc tatgaaatga acgcaacata tagaaatttc atgtggacaa 480
cgacatttag acggtatctt aattagaccg attaattagt aatatactta tatatataat 540
tagtggtgat tataagttta cttatccact tgagaattta aacaatgggc aataccttaa 600
tgtcgaaaga agccgtcccc acttcgtgta atgagttatg ggggagagat cctgttaaat 660
cgtcaaataa aacaacttaa gaactagaaa ttgacaccaa aaatcataaa gagaacgttg 720
aagaagtcac ttatcgtatc cagctcatat ttcttagcta agatcaaac aaggccgttg 780
aaagggttg taagaaaatg tcgaagaaac cgtgggggtt agaagaaaga caagaaatag 840
aagaacaatg atgttaaatt gcctattttg gtgtatagga gttgtcaaaa gaggagagag 900
agaagaaaat taggtcaaaa taatgagcac taaaaatgga gacatgtgtt gagtaactat 960
tacaagagcg acttatgctt ctttatggca atgatatcca aaccaaagtg caacgctcct 1020
tttttgccct aatttcgtaa agtctctctc cttcttcgtc cttaggaaaa accctagaaa 1080
tttaatccct tgttcttgat cttgcttttt gagtaaccat gattttgacc acacactatt 1140
tcttctatct tttgtggtct ataggatttt gctttatatg tgtttcttgt attgctccgt 1200
acgtacgtat acgaatttaa atggttataa caaggtttat ataaactagc acaaatgagt 1260
ccatgaaatt tgtagcgaa aaaggtagaa atatatgag tctttaaacg gcaatatata 1320
taattttgct gcaaaactta gctttaatca tgatctaata atattttctt taatttcctt 1380
tgccaaatta atcacatgca cggatttttg gcaagttatg tgtogaattc ttccattcac 1440
acaacactaa acttaattag aactctagga aatattttta aatgacaact ttatcgaaaa 1500
aaatttagtt atgaaaacaa ttccagaatt aaacatgagc tatataattt aagataaaat 1560
gaagtaatat tgatatgtat gtaataacat atctgattgc ggtaaaaaaa aacatatctg 1620

```

attaaattgt tcatgcaggc ccatgtcact atgatgtcat cacgttttta ttttcacaat 1680
 aactaatata tattcaaaaa aatagttttg tcagattaaa ttttttttgg tggtcagctt 1740
 tctccaacct actaaactag tttggaatgt tctcttcttt attttttctt ttcttgattt 1800
 cttatgtttt ttatttatgg aattttaaga cggattgttt aggtcgtttc tctcttttct 1860
 tgttttctaa agttactttt gtaaactcat ctctcccaa ttagacagtc aatcatatag 1920
 ttatctttta atatatgtct agttgataaa aaaaaatgaa aaatactggg ggtagttcta 1980
 ctaatgtttg tgtaaaaaat ctgatattat gaatctaac aatttctttg atcgtataat 2040
 gtgggttaaa tttagtaatt ttttacataa ataagaactg taatgttgat gtatattggg 2100
 gaatcagtat attagcttgg gtaactatac ttctggaaat acttgaagat ttaactattt 2160
 gcaaaattat aatttagtcc cgaaaaatac agacgacggg acacgacaac atataagcag 2220
 gtttgaatct tggaaaattt tgtatacata acctatataa atactaatgt tctggttggg 2280
 ttcaaaagcc ttttcaaaag ttccattttt taaattcaag gacattttac ataggaaata 2340
 agttgagtca taaaaataa tggttatttt gtaaggtttt ttttttgatt aaaacgcaca 2400
 tattaagaag ttagtttttt ttactacca aatatcaatt aattttaaac catgcaacca 2460
 ttcataaaac aatactatta aagaatataa ataatacaca aatattaaat acacttaaaa 2520
 tttacatata aatttacaaa acatctaatt aattgaaaca gaaaggaaaa ggtaaaatat 2580
 atcataaaat gagacatata tcctataaaa aaaaaatgag gcatatgaag taaataataa 2640
 gagacatgca tgtaagcatt cggttaatta atcgagtcaa agatatatat cagtaaatac 2700
 atatgtgtat atttctggaa aaagaatata tatattgaga aataagaaaa gatgaaa 2757
 atg gaa aat ggt atg tat aaa aag aaa gga gtg tgc gac tct tgt gtc 2805
 Met Glu Asn Gly Met Tyr Lys Lys Lys Gly Val Cys Asp Ser Cys Val
 1 5 10 15
 tcg tcc aaa agc aga tcc aac cac agc ccc aaa aga agc atg atg gag 2853
 Ser Ser Lys Ser Arg Ser Asn His Ser Pro Lys Arg Ser Met Met Glu
 20 25 30
 cct cag cct cac cat ctc ctc atg gat tgg aac aaa gct aat gat ctt 2901
 Pro Gln Pro His His Leu Leu Met Asp Trp Asn Lys Ala Asn Asp Leu
 35 40 45
 ctc aca caa gaa cac gca gct ttt ctc aat gat cct cac cat ctc atg 2949
 Leu Thr Gln Glu His Ala Ala Phe Leu Asn Asp Pro His His Leu Met
 50 55 60
 tta gat cca cct ccc gaa acc cta att cac ttg gac gaa gac gaa gag 2997
 Leu Asp Pro Pro Pro Glu Thr Leu Ile His Asp Glu Asp Glu Glu
 65 70 75 80
 tac gat gaa gac atg gat gcg atg aag gag atg cag tac atg atc gcc 3045
 Tyr Asp Glu Asp Met Asp Ala Met Lys Glu Met Gln Tyr Met Ile Ala
 85 90 95

gtc atg cag ccc gta gac atc gac cct gcc acg gtc cct aag ccg aac 3093
 Val Met Gln Pro Val Asp Ile Asp Pro Ala Thr Val Pro Lys Pro Asn
 100 105 110

cgc cgt aac gta agg ata agc gac gat cct cag acg gtg gtt gct cgt 3141
 Arg Arg Asn Val Arg Ile Ser Asp Asp Pro Gln Thr Val Val Ala Arg
 115 120 125

cgg cgt cgg gaa agg atc agc gag aag atc cga att ctc aag agg atc 3189
 Arg Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Ile
 130 135 140

gtg cct ggt ggt gcg aag atg gac aca gct tcc atg ctc gac gaa gcc 3237
 Val Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala
 145 150 155 160

ata cgt tac acc aag ttc ttg aaa cgg cag gtg agg att ctt cag cct 3285
 Ile Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Ile Leu Gln Pro
 165 170 175

cac tct cag att gga gct cct atg gct aac ccc tct tac ctt tgt tat 3333
 His Ser Gln Ile Gly Ala Pro Met Ala Asn Pro Ser Tyr Leu Cys Tyr
 180 185 190

tac cac aac tcc caa ccc tga tgaactacac agaagctcgc tagctagaca 3384
 Tyr His Asn Ser Gln Pro
 195

tttgggtgtca tcctctcaac ctttttcatg ttgatataatt atatatagat gcataaagat 3444
 tccgatccaag attgtatggg tgttttaata ttattattct aagatatatg atgtacaatt 3504
 gtgtaccaag tttctttatc ttgatatcat atgcataaat aattggtgaa taaaaagaag 3564
 atattgattg taaacaaaaa aaagaagata ttgattgtta attagggttt gatcattctg 3624
 tatgaaagct ttggcctgca aattaatttt cgatatatat atatatatat ggagaatata 3684
 tatcaaatac ttttttaatt tgactataat ttgtatcaat tatctgaatc tgatgagtgt 3744
 aggttatata tggattagca aaaaagaaaa caaccattat tacgcaccta cattaaaaat 3804
 catccaccaa agaagaaacc atcctcaaga gggttccc 3842

<210> 25

<211> 198

<212> PRT

<213> Arabidopsis sp.

<400> 25

Met Glu Asn Gly Met Tyr Lys Lys Lys Gly Val Cys Asp Ser Cys Val
 1 5 10 15
 Ser Ser Lys Ser Arg Ser Asn His Ser Pro Lys Arg Ser Met Met Glu
 20 25 30
 Pro Gln Pro His His Leu Leu Met Asp Trp Asn Lys Ala Asn Asp Leu
 35 40 45
 Leu Thr Gln Glu His Ala Ala Phe Leu Asn Asp Pro His His Leu Met
 50 55 60
 Leu Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp Glu Glu
 65 70 75 80

